

RESULT 1

A26772

Photinus-luciferin 4-monoxygenase (ATP-hydrolysing) (EC 1.13.12.7) [similarity] - com
 N;Alternate names: firefly luciferase
 C;Species: Photinus pyralis (common eastern firefly)
 C;Date: 19-Nov-1988 #sequence_revision 20-Aug-1994 #text_change 09-Jul-2004
 C;Accession: A26772
 R;de Wet, J.R.; Wood, K.V.; DeLuca, M.; Helinski, D.R.; Subramani, S.
Mol. Cell. Biol. 7, 725-737, 1987
 A;Title: Firefly luciferase gene: structure and expression in mammalian cells.
 A;Reference number: A26772; MUID:87144243; PMID:3821727
 A;Accession: A26772
 A;Molecule type: DNA
 A;Residues: 1-550
 A;Cross-references: UNIPROT:P08659; UNIPARC:UPI0000038BE4; GB:M15077; NID:g160793; PID
 A;Note: the authors translated the codon CAA for residue 134 as Glu
 C;Comment: This protein catalyzes the oxidation of luciferin in the presence of ATP, o
 C;Genetics:
 A;Introns: 42/3; 112/1; 223/2; 330/2; 448/3; 504/1
 C;Superfamily: 4-coumarate-CoA ligase; acetate-CoA ligase homology
 C;Keywords: ATP; luminescence; monooxygenase; oxidoreductase
 F;71-535/Domain: acetate-CoA ligase homology
 F;548-550/Region: peroxisome/glyoxysome location signal (S-[RKH]-L) motif .

Alignment Scores:

Pred. No.:	6.44e-170	Length:	550
Score:	2806.00	Matches:	544
Percent Similarity:	99.6%	Conservative:	1
Best Local Similarity:	99.5%	Mismatches:	2
Query Match:	82.9%	Indels:	0
DB:	1	Gaps:	0

US-10-664-341-72 (1-1830) x A26772 (1-550)

Qy	1 ATGGCCGATGCTAAGAACATTAAAGAAGGCCCTGCTCCCTTCTACCCCTCTGGAGGATGGC 60
Db	1 MetGluAspAlaLysAsnIleLysLysGlyProAlaProPheTyrProLeuGluAspGly 20
Qy	61 ACCGCTGGCGAGCAGCTGCACAAGGCCATGAAGAGGTATGCCCTGGTGCCCTGGCACCATTT 120
Db	21 ThrAlaGlyGluGlnLeuHisLysAlaMetLysArgTyrAlaLeuValProGlyThrIle 40
Qy	121 GCCTTCACCGATGCCCACATTGAGGTGGACATCACCTATGCCGAGTACTCGAGATGTCT 180
	:::
Db	41 AlaPheThrAspAlaHisIleGluValAsnIleThrTyrAlaGluTyrPheGluMetSer 60
Qy	181 GTGCGCCTGGCCGAGGCCATGAAGAGGTACGGCCTGAACACCAACCACCGCATCGTGGTG 240
Db	61 ValArgLeuAlaGluAlaMetLysArgTyrGlyLeuAsnThrAsnHisArgIleValVal 80
Qy	241 TGCTCTGAGAACTCTCTGCAGTTCTTCATGCCAGTGCTGGCGCCCTGTTCATCGGAGTG 300
Db	81 CysSerGluAsnSerLeuGlnPhePheMetProValLeuGlyAlaLeuPheIleGlyVal 100
Qy	301 GCCGTGGCCCTGCTAACGACATTACAACGAGCGCGAGCTGCTGAACAGCATGGGCATT 360
Db	101 AlaValAlaProAlaAsnAspIleTyrAsnGluArgGluLeuLeuAsnSerMetAsnIle 120
Qy	361 TCTCAGCCTACCGTGGTGTTCGTGTCTAACGAGGCCCTGCAGAACAGATCCTGAACGTGCAG 420
Db	121 SerGlnProThrValValPheValSerLysLysGlyLeuGlnLysIleLeuAsnValGln 140

Qy	421 AAGAAGCTGCCTATCATCCAGAAGATCATCATCATGGACTCTAACGACCGACTACCAGGGC 480
Db	141 LysLysLeuProIleIleGlnLysIleIleIleMetAspSerLysThrAspTyrGlnGly 160
Qy	481 TTCCAGAGCATGTACACATTGTGACATCTCATTCGCTCCTGGCTTAACGAGTACGAC 540
Db	161 PheGlnSerMetTyrThrPheValThrSerHisLeuProProGlyPheAsnGluTyrAsp 180
Qy	541 TTCGTGCCAGAGTCTTCGACAGGGACAAAACCATTGCCCTGATCATGAACAGCTCTGGG 600
Db	181 PheValProGluSerPheAspArgAspLysThrIleAlaLeuIleMetAsnSerSerGly 200
Qy	601 TCTACCGGCCTGCCTAACGGCGTGGCCCTGCCTCATCGCACCGCCTGTGTGCGCTTCT 660
Db	201 SerThrGlyLeuProLysGlyValAlaLeuProHisArgThrAlaCysValArgPheSer 220
Qy	661 CACGCCCGCAGCCCTATTTCCGCAACCAGATCATCCCCGACACCGCTATTCTGAGCGTG 720
Db	221 HisAlaArgAspProIlePheGlyAsnGlnIleIleProAspThrAlaIleLeuSerVal 240
Qy	721 GTGCCATTCCACCACGGCTTCGGCATGTTACCACCCCTGGGCTACCTGATTGCGGGCTT 780
Db	241 ValProPheHisHisGlyPheGlyMetPheThrThrLeuGlyTyrLeuIleCysGlyPhe 260
Qy	781 CGGGTGCTGATGTACCGCTTCGAGGAGGAGCTGTTCTGCGCAGCCTGCAAGACTAC 840
Db	261 ArgValValLeuMetTyrArgPheGluGluGluLeuPheLeuArgSerLeuGlnAspTyr 280
Qy	841 AAAATTCACTGCCCTGCTGGTGCCAACCCTGTTAGCTTCAGCTTCGCTAACGACCCCTG 900
Db	281 LysIleGlnSerAlaLeuLeuValProThrLeuPheSerPhePheAlaLysSerThrLeu 300
Qy	901 ATCGACAAGTACGACCTGTCTAACCTGCACGAGATTGCCCTGGCGGCCACTGTCT 960
Db	301 IleAspLysTyrAspLeuSerAsnLeuHisGluIleAlaSerGlyGlyAlaProLeuSer 320
Qy	961 AAGGAGGTGGCGAAGCCGTGGCCAAGCGCTTCATCTGCCAGGCATCCGCCAGGGCTAC 1020
Db	321 LysGluValGlyGluAlaValAlaLysArgPheHisLeuProGlyIleArgGlnGlyTyr 340
Qy	1021 GGCCTGACCGAGACAACCAGCGCCATTCTGATTACCCCAGAGGGCGACGACAAGCCTGGC 1080
Db	341 GlyLeuThrGluThrThrSerAlaIleLeuIleThrProGluGlyAspAspLysProGly 360
Qy	1081 GCCGTGGCAAGGTGGTGCCATTCTCGAGGCCAAGGTGGTGGACCTGGACACCGGCAAG 1140
Db	361 AlaValGlyLysValValProPhePheGluAlaLysValValAspLeuAspThrGlyLys 380
Qy	1141 ACCCTGGAGTGAACCAGCGCGCGAGCTGTGTGCGCGGCCCTATGATTATGTCCGGC 1200
Db	381 ThrLeuGlyValAsnGlnArgGlyGluLeuCysValArgGlyProMetIleMetSerGly 400
Qy	1201 TACGTGAATAACCCTGAGGCCACAAACGCCCTGATCGACAAGGACGGCTGGCTGCAC 1260
Db	401 TyrValAsnAsnProGluAlaThrAsnAlaLeuIleAspLysAspGlyTrpLeuHisSer 420
Qy	1261 GGCGACATTGCCTACTGGGACGAGGACGAGCACTTCTCATCGTGGACGCCCTGAAGTCT 1320
Db	421 GlyAspIleAlaTyrTrpAspGluAspGluHisPhePheIleValAspArgLeuLysser 440

Qy	1321	CTGATCAAGTACAAGGGCTACCAGGTGGCCCCAGCCGAGCTGGAGTCTATCCTGCTGCAG	1380
Db	441	LeuIleLysTyrLysGlyTyrGlnValAlaProAlaGluLeuGluSerIleLeuLeuGln	460
Qy	1381	CACCCATAACATTTCGACGCCGGAGTGGCCGGCCTGCCGACGACGATGCCGGCGAGCTG	1440
Db	461	HisProAsnIlePheAspAlaGlyValAlaGlyLeuProAspAspAspAlaGlyGluLeu	480
Qy	1441	CCTGCCGCCGTCGTCGTGCTGGAACACGGCAAGACCATGACCGAGAAGGAGATCGTGGAC	1500
Db	481	ProAlaAlaValValLeuGluHisGlyLysThrMetThrGluLysGluIleValAsp	500
Qy	1501	TATGTGGCCAGCCAGGTGACAACCGCCAAGAACGCTGCGCGGAGTGGTGTTCGTGGAC	1560
Db	501	TyrValAlaSerGlnValThrThrAlaLysLysLeuArgGlyGlyValValPheValAsp	520
Qy	1561	GAGGTGCCAAGGGCTGACCGCAAGCTGGACGCCGCAAGATCCGCGAGATCCTGATC	1620
Db	521	GluValProLysGlyLeuThrGlyLysLeuAspAlaArgLysIleArgGluIleLeuIle	540
Qy	1621	AAGGCTAAGAAAGGCGGCAAG	1641
Db	541	LysAlaLysLysGlyGlyLys	547